

Breakdown of self-averaging in the Bose glass

Anthony Hegg¹, Frank Krüger², and Philip W. Phillips¹

¹*Department of Physics, University of Illinois, 1110 West Green Street, Urbana, Illinois 61801, USA*

²*SUPA, School of Physics and Astronomy, University of St. Andrews, St. Andrews, KY16 9SS, United Kingdom*

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We study the square-lattice Bose-Hubbard model with bounded random on-site energies at zero temperature. Starting from a dual representation obtained from a strong-coupling expansion around the atomic limit, we employ a real-space block decimation scheme. This approach is non-perturbative in the disorder and enables us to study the renormalization-group flow of the induced random-mass distribution. In both insulating phases, the Mott-insulator and the Bose glass, the average mass diverges, signaling short range superfluid correlations. The relative variance of the mass distribution distinguishes the two phases, renormalizing to zero in the Mott insulator and diverging in the Bose glass. Negative mass values in the tail of the distribution indicate the presence of rare superfluid regions in the Bose glass. The breakdown of self-averaging is evidenced by the divergent relative variance, increasingly non-Gaussian distributions, and a correlation-length exponent $\nu = 0.6 \pm 0.05$ that violates the Harris-criterion bound.

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Introducing quenched disorder into an otherwise pure system can lead to subtle and complex results and the disordered Bose-Hubbard (BH) model is no exception. While the clean BH model shows a relatively straightforward bosonic competition between repulsion and tunneling, the disordered model exhibits a new gapless insulating phase, the Bose glass (BG), the precise location of which has proven problematic from the outset [1]. With the advent of experimental methods that can engineer this model directly [2], the problem has been inverted and this has sparked renewed interest in the role disorder plays in quantum systems.

In this Letter, we develop a non-perturbative method to probe the nature of the transition between the localization-induced BG and the Mott insulator (MI) in the two-dimensional BH model with bounded potential disorder. The MI arises from the on-site repulsions and hence dominates in the limit the hopping vanishes while the superfluid (SF) is the ground state in the opposite regime. It is in the difficult intermediate parameter space where the BG phase obtains. Fisher and colleagues [1] argued that the BG is a quantum Griffiths phase dominated by arbitrarily large SF regions that are, however, exponentially suppressed. Despite the abundance of numerical [3–9] and analytical [10–20] work on the subject, it is only recently that several aspects of this model have been fully understood, such as confirmation that the BG always intervenes between MI and SF phases [21] (see Fig. 1) and the distinction between the MI and BG regarding whether fluctuations are self-averaging [22].

As argued by Aharony and Harris [23], the breakdown of self-averaging can be identified from the renormalization-group (RG) flow of the relative variance of any extensive variable. If the relative variance does not renormalize to zero, the central limit theorem no longer applies and the system is not self-averaging. This concept has been used to characterize the phase transition

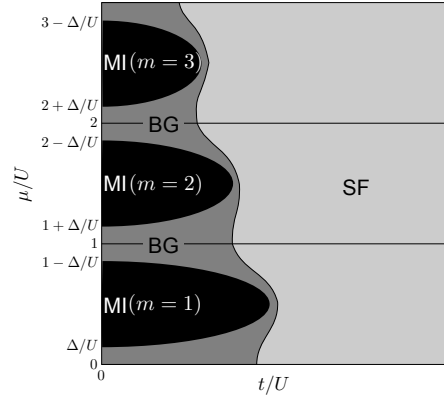


FIG. 1: Sketch of the phase diagram for the disordered Bose-Hubbard model as a function of the hopping t/U and chemical potential μ/U in units of the on-site repulsion U . Random shifts in the on-site energies bounded by $\Delta < U/2$ lead to the formation of a compressible Bose-glass (BG) phase, separating the Mott-insulating (MI) lobes from the superfluid (SF).

between the MI and the BG [22] within a disorder averaged Replica field theory which is valid close to the atomic strong-coupling limit. In both insulating phases, the mass of the theory diverges, signaling the presence of short-ranged SF correlations. Since in dimensions $d < 4$ the variance of the mass distribution diverges as well, the breakdown of self-averaging can be readily understood as a competition between the spread of the distribution versus the shift of its average. In the MI, the shift dominates the spread leading to a vanishing relative variance. In the BG, the spread is faster and the relative variance diverges. This characterization of the MI to BG transition is consistent with the commonly accepted picture that the BG is dominated by rare SF regions since the negative mass values occur in the tail of the distribution. Whether the onset of this Griffiths-type instability is cor-

rectly described by an RG calculation that is perturbative in the disorder remains a central question.

We address this question within a real-space block decimation RG scheme on a $d = 2$ dimensional square lattice. This approach is non-perturbative in the disorder and hence enables a study of the RG flow of the full random-mass distribution, a necessity for any definitive statement about Griffiths-type physics to be made. Our results confirm that the relative variance serves as the order parameter for the MI-to-BG transition. Determining the correlation length from the scale at which the relative variance becomes of order one, we extract a correlation-length exponent $\nu = 0.6 \pm 0.05$ which is close to the analytical value $\nu = 1/d$ obtained within the perturbative 1-loop RG [22]. It has been argued [23, 24] that a violation of the Harris-criterion bound $\nu \geq 2/d$ for critical disordered systems [25, 26] is indicative of the lack of self-averaging. The absence of the central-limit theorem in the BG is further evidenced by an increasingly non-Gaussian shape of disorder distributions.

Our starting point is the simplest form of the disordered BH model on a square lattice,

$$\mathcal{H} = -t \sum_{\langle i,j \rangle} (b_i^\dagger b_j + b_j^\dagger b_i) - \sum_i \mu_i \hat{n}_i + \frac{U}{2} \sum_i \hat{n}_i (\hat{n}_i - 1), \quad (1)$$

which describes bosons tunneling with amplitude t between nearest-neighbor sites i and j and interacting via an on-site repulsion U . The bosonic raising and lowering operators are given by b_i^\dagger, b_i respectively where $\hat{n}_i = b_i^\dagger b_i$ is the bosonic number operator. μ_i is the chemical potential shifted by the on-site disorder potential, $\mu_i = \mu - \epsilon_i$. The random site energies ϵ_i are uncorrelated between different sites and uniformly distributed in the interval $[-\Delta, \Delta]$. From minimization of the energy in the atomic limit it is straightforward to see that for $\Delta < U/2$ the phase diagram retains MI phases (see Fig. 1).

To facilitate a strong coupling expansion we follow the standard procedure [27, 28]. After expressing the model by a coherent-state path integral in imaginary time, we decouple the hopping term by a Hubbard-Stratonovich transformation and trace over the original boson fields. We then perform a temporal gradient expansion to obtain the effective dual action on a lattice,

$$S_{\text{eff}} = a^2 \sum_i \int d\tau \left(\frac{1}{2} \sum_\delta T_{i\delta} |\psi_\delta - \psi_i|^2 + K_i^{(1)} \psi_i^* \partial_\tau \psi_i + K_i^{(2)} |\partial_\tau \psi_i|^2 + R_i |\psi_i|^2 + H_i |\psi_i|^4 \right), \quad (2)$$

where a denotes the lattice spacing and the sum over δ runs over the nearest neighbors of site i . By construction, the complex fields correspond to the SF order parameter $\psi_i \sim \langle b_i \rangle$. In regions where $R_i > 0$, SF order is suppressed. The mass R_i therefore corresponds to the local

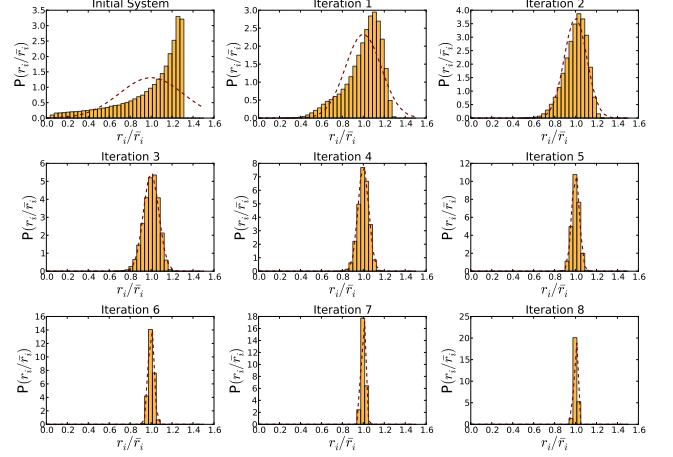


FIG. 2: RG flow of the mass distribution $P(r_i/\bar{r}_i)$ normalized to a mean of 1 in the MI. Starting with the initial distribution given by Eq. (3a), each subplot represents the probability distribution of this quantity after another iteration of the RG equations. We see that the Gaussian fit (red dotted line) becomes better with successive iterations. In addition, the width of the distribution, which corresponds to the relative variance, narrows.

Mott gap. The calculation of the coupling constants as a function of the microscopic parameters of the BH model is straightforward, e.g. R_i and H_i are related to the single- and two-particle bosonic Green functions of the local on-site Hamiltonian, respectively, while the temporal gradient terms $K_i^{(1)}$ and $K_i^{(2)}$ are given by derivatives of the mass with respect to the chemical potential. We specialize to the first Mott lobe with $m = 1$ bosons per site in which the coefficients are given by [19, 28]

$$R_i = \frac{1}{zt} - \left(\frac{2}{U - \mu_i} + \frac{1}{\mu_i} \right), \quad (3a)$$

$$K_i^{(1)} = -\frac{\partial R_i}{\partial \mu_i}, \quad K_i^{(2)} = -\frac{1}{2} \frac{\partial^2 R_i}{\partial \mu_i^2}, \quad (3b)$$

$$H_i = \left(\frac{2}{U - \mu_i} + \frac{1}{\mu_i} \right) \left(\frac{2}{(U - \mu_i)^2} + \frac{1}{\mu_i^2} \right) - \frac{6}{(U - \mu_i)^2 (3U - 2\mu_i)}, \quad (3c)$$

where $z = 2d = 4$ is the coordination number of the square lattice. In the clean limit, $\mu_i = \mu$, the mean-field phase boundary between the first MI lobe and the SF is obtained from $R(\mu, t, U) = 0$. In the presence of disorder, $\mu_i = \mu - \epsilon_i$, the coefficients $R_i, K_i^{(1)}, K_i^{(2)}$, and H_i depend on the disorder potential ϵ_i , which induces non-trivial disorder distributions of the coefficients. Note that initially the dual hopping amplitudes $T_{i\delta} = 1/(za^2t)$ are uniform. We allow for a spatial dependence of the hopping since disorder will be induced under block decimation.

Equations (3) provide the initial conditions for our pro-

cedure where the random on-site energies are generated from a uniform distribution on the interval $[-\Delta, \Delta]$. In order to determine the phase for a given set of parameters t , U , μ , and Δ of the disordered BH model (1), we derive a set of recursion equations using block decimation.

We start with the discrete action (2) and eliminate short-range degrees of freedom by integrating out every other site, treating the quartic terms H_i perturbatively to leading order. The remaining points form a new square lattice with lattice spacing $a' = \sqrt{2}a$ and tilted 45° from the original system. A second iteration of this procedure brings the system back to the original angle with appropriate reindexing. Recollecting the resulting terms and rescaling the action to look like the original, we find the RG recursion equations to be

$$R'_{i'} = R_i + \sum_{\delta} T_{i\delta} - \sum_{\delta, \delta'} T_{i\delta} T_{i\delta'} I_{\delta} \left(1 - 4H_i \tilde{I}_{\delta} I_{\delta}\right) \quad (4a)$$

$$T'_{i'j'} = \sum_{\epsilon, \epsilon'} T_{\epsilon} T_{\epsilon'} I_{\epsilon\epsilon'} \left(1 - 4H_{\epsilon\epsilon'} \tilde{I}_{\epsilon\epsilon'} I_{\epsilon\epsilon'}\right), \quad (4b)$$

where $I_i = (R_i + \sum_{\delta} T_{i\delta})^{-1}$ is the static propagator and $\tilde{I}_i = \left(4(R_i + \sum_{\delta} T_{i\delta})K_i^{(2)} + (K_i^{(1)})^2\right)^{-\frac{1}{2}}$. The indices δ and δ' correspond to nearest neighbors of site i , whereas ϵ and ϵ' correspond to the bonds adjacent to the bond connecting the sites i' and j' of the remaining lattice. The site $\epsilon\epsilon'$ is the common vertex of the bonds ϵ and ϵ' (see Fig. 3). Since we are interested in the MI to BG transition at incommensurate filling, we can neglect any corrections to the coefficients $K^{(1)}$, $K^{(2)}$, and H beyond dimensional scaling. The dynamic exponent is $d_z = 2$ since $K_i^{(1)} \neq 0$ except for a vanishing subset of sites of zero measure.

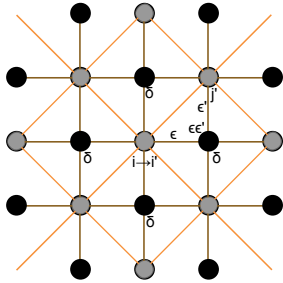


FIG. 3: Illustration of the block decimation scheme underlying the recursion relations (4).

From Eq. (4b) it is obvious that the gradient terms are renormalized under block decimation. The effective mass should therefore be defined relative to the kinetic hopping terms. In the following, we will use the effective local mass variable

$$r_i := zR_i / \sum_{\delta} T_{i\delta}. \quad (5)$$

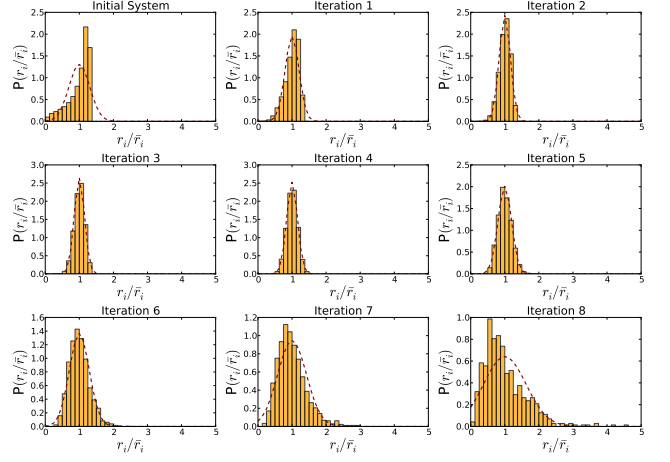


FIG. 4: RG flow of the mass distribution $P(r_i/\bar{r}_i)$ in the BG. Note the similarity to Fig. 2 up to an overall displacement in the first histogram. Here we see the Gaussian fit becomes worse and worse due to the long tail of the distribution. This corresponds to an increasing relative variance.

As a consistency check, we evaluate our recursion relations in the clean limit. For $T = T_{i\delta}$, $R = R_i$, and $H = H_i = 0$, the RG equations (4) reduce to $R' = R + 4T - 16T^2/(R + 4T)$ and $T' = 4T^2/(R + 4T)$, leading to the recursion relation $r' = 2r + r^2/4$ for the effective mass. This indeed correctly describes the mean-field transition between the MI and the SF at $r = 0$.

In the following, we integrate the RG equations (4) numerically for the inhomogeneous system obtained for one particular disorder realization and keep track of the values of the coupling constants on each lattice site. This allows us to extract the mass distribution $P(r_i)$ at each iteration step of the block decimation. While we vary the hopping t/U and the lattice constant a to tune through the MI-to-BG transition, we use the same values $\Delta/U = 0.1$ for the disorder strength and $\mu/U = 0.15$ for the chemical potential throughout the paper. Since Eq. (2) has only nearest neighbor or on-site terms, we can ignore the boundary points after each iteration without affecting the overall distribution. The major limitation to this method is the necessity of finite size lattices. Estimates of any diverging quantities near the critical point must take into account finite system size effects. Accompanying this limitation is the computation time increase for correspondingly larger system sizes. In the data given below we use an initial square grid of points with side length $L = 506$ sites.

As expected for insulating phases, in both the MI and the BG, the mean \bar{r}_i of the mass distribution increases exponentially under the RG signaling short-range SF correlations. To distinguish the behavior in the MI and the BG, we normalize to a mean of unity and analyze the evolution of $P(r_i/\bar{r}_i)$. The variance of this rescaled distribution corresponds to the relative variance of the mass

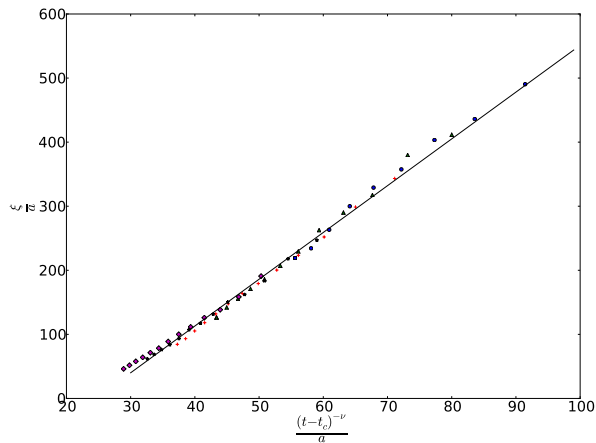


FIG. 5: Scale collapse of the correlation length plotted as a power law of the reduced hopping. The fitting parameters are t_c and ν . This fit corresponds to the least square error confirming $\nu = 0.6 \pm 0.05$.

distribution, which should serve as order parameter [22].

In Fig. 2 the RG flow of $P(r_i/\bar{r}_i)$ in the MI phase is shown. Note that the initial mass distribution is asymmetric and non-Gaussian due to the functional dependence (3a) on the uniformly distributed on-site energies ϵ_i . As a consequence of the relatively small hopping value t/U , the bulk of the sites begin well above $r_i = 0$ and continue together towards larger values under repeated iteration. Increasing the number of iterations results in a distribution well described by a Gaussian. Further, the width of the distribution narrows, indicating a vanishing relative variance. This demonstrates that in the MI disorder is irrelevant and the system is self-averaging.

The situation changes dramatically as we increase the value of t/U and enter the BG phase (see Fig. 4). While the overall shape of the initial distribution looks quite similar to the one in the MI, now a large fraction of the initial sites lies close to or below $r_i = 0$. With enough sites close to the transition point, some regions of the system take much longer to flow to large positive values than others. This results in a drastic spread of values upon repeated iteration of the RG, leading to a divergence of the relative variance. In addition, the distribution develops a non-Gaussian form under successive iterations, indicating a violation of the central limit theorem. This demonstrates a breakdown of self-averaging in the BG.

Our results show that the relative variance of the random-mass distribution r_i serves as an order parameter for the transition between the MI and the BG. We can therefore determine a correlation length $\xi/a = \sqrt{2}^{n_c}$ in the BG from the average number of iterations it takes before the relative variance becomes of order unity. For the parameters used in Fig. 4 this happens between 6 and 7 iterations. A more precise value is obtained by averaging over several disorder realizations. Note that once the relative variance becomes of order unity, the left tail

of the distribution pushes through zero. Therefore, the correlation length ξ corresponds to the typical distance between SF droplets in the system.

At the transition to the MI we expect the correlation to diverge as a power law $\xi \propto (t - t_c)^{-\nu}$. To extract the correlation-length exponent ν , we vary the hopping slightly above the transition point for a fixed value of the initial lattice spacing a and extract the correlation length as described above by averaging over several disorder realizations. In the following, we use lattice constants $a = 0.2, 0.25, 0.3, 0.35, 0.4$ and average over 10-20 disorder realizations for each value. Note that the value t_c of the transition point is non-universal and depends on a . As shown in Fig. 5, plotting ξ/a vs $[t - t_c(a)]^{-\nu}/a$, the different data sets collapse on a single straight line for $\nu = 0.6 \pm 0.05$. This value violates the Harris criterion bound $\nu \geq 2/d$ [25, 26] but is consistent with a breakdown of self-averaging [23, 24].

Discussion and Conclusion. We used a real-space block decimation method to characterize the MI-to-BG transition of the disordered BH model. By analyzing the RG flow of the induced random-mass distribution in the dual field theory, we have demonstrated that the transition is characterized by a breakdown of self-averaging. The associated correlation length corresponds to the typical separation of rare SF regions. Our work provides the first explicit confirmation that the instability towards the formation of the BG is of the Griffith type.

The method employed here is fundamentally non-perturbative in the strength of the disorder and enables us to study the RG flow of entire disorder distributions, whereas the perturbative 1-loop momentum-shell RG based on the disorder averaged replica theory is restricted to the mean and the variance of the random mass distribution [22]. Both approaches, however, show that the relative variance diverges in the BG. This is an important result as it demonstrates that contrary to the general belief, the onset of Griffith instabilities is captured in perturbative RG. The comparison of the correlation-length exponents obtained by the two methods suggests that corrections beyond 1-loop order are small.

The real-space RG approach presented here has a wide range of future applications. It can be used to study the effects of spatial correlations in the disorder and entails the search for self-similar disorder characterized by scale invariant distribution functions. Finally, the method is not restricted to disorder distributions, but can be used to study other inhomogeneities such as the so-called wedding cake structures of alternating MI and SF regions found in optical-lattice system [29].

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